STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/542,937_

Source: _PG/10_

Date Processed by STIC: _7/29/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.2.2 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/542,937_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _√_ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _√_ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

[Handwritten: IMPORTANT! see item 4 on Error summary sheet]
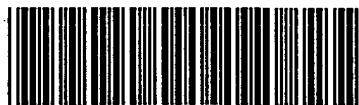
[Handwritten: Do NOT use bold print]

PCT

[Handwritten: see pp 1-4]

RAW SEQUENCE LISTING   DATE: 07/29/2005
PATENT APPLICATION: US/10/542,937   TIME: 08:45:53

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\07292005\J542937.raw**

[Handwritten: do you mean "method"?]

```
       3 <110> APPLICANT: EFARMES, S.A.
W-->   4 <120> TITLE OF INVENTION: Device a meted for detecting low density lipoprotein
receptor gene
W-->   5        mutations
W-->   6        associated with familial hypercholesterolemia
W-->   7 <130> FILE REFERENCE: PCT-154
C-->   8 <140> CURRENT APPLICATION NUMBER: US/10/542,937
C-->   8 <141> CURRENT FILING DATE: 2005-07-21
W-->   8 <160> NUMBER OF SEQ ID: 259
W-->   9 <150> PRIOR APPLICATION NUMBER: ES200300206
W-->  10 <151> PRIOR FILING DATE: 28.01.03
W-->  11 <150> PRIOR APPLICATION NUMBER: ES200302671
W-->  12 <151> PRIOR FILING DATE: 17.11.03
```

[Handwritten: use this date format]
[Handwritten stamp: Does Not Comply / Corrected Diskette Needed]
[Handwritten: 2003-01-28]
[Handwritten: 2003-11-17]

[Handwritten: <160> 259 <-- move this under last <151> do NOT use alphabetical headings]

ERRORED SEQUENCES

```
E-->  13 <210>            SEQ ID NO: 1
      14 <211> LENGTH: 60.000
E-->  15 <212> TYPE: polynucleotide
      16 <213> ORGANISM: human
W-->  17 <220> FEATURE:
      18 <221> NAME/KEY: gene
      19 <223> OTHER INFORMATION: rLDL
W-->  20 <400> SEQUENCE:
```

[Handwritten: 60000) invalid response. The only valid <212> responses are DNA, RNA, or PRT]

[Handwritten: <-- insert the sequence number]

```
      22 aaaagatggt gtatccattc aatggaacat tatttggcct ttaaaaggaa ggaaattctc 60
      23 actgagcata gtggtttatg cctgtaatcc cagcactttg ggaggctgag gcaggggga 120
      24 ggggggcggtt cacctgaggt caggagttca agaccagcct ggccaacatg gtgaaatccc 180
      25 gtctctacta aaaatacaaa aaaattagcc gagtgtggtg gcacacacct gtaagccagg 240
      26 ctacacggga gactgaggca ggagaatcgc tggaacccgg.gaggcagagg ctgcagagag 300
      27 ccgagattgc gtcactgcac tccagcctgg gtgacagagc gagactcttg tcttaaaaaa 360
      28 aaaaagaagg aaggaaggaa ggaaggaagg aagttctgac acaggctcca acacagatgt 420
      29 tatgctcagt gaaataagcc agacatgaaa ggacaaatac tgcctgatct cattcataag 480
      30 aggtccctag aattgtagaa tggtgtgtgc cacgggctgg gaggggtgt ggccagagtt 540
      31 tcagtttggg aagttgagaa tgttctggag atggatggcg gtagtggtgg ttgcacaact 600
      32 gtgtgaatgc gcttaatgcc tctgaattgt gcagttacaa gtggttcgga tgggccgggc 660
      33 gcggtggctc atgcctgtaa tcccagcact ttgggaggcc gaggcaggtg gatcatgaga 720
      34 tcaggagatc gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaaataca 780
      35 aaaaattagc caggcatggt ggtgggcacc tgtagtccca gctacttggg aggcggaggc 840
      36 aggagaatgg cgtgaacacg ggaggcagaa cttgcagtga gccgagatca cgccactgca 900
      37 ctccagcctg ggcgacagag tgagactccg tctaaaaaaa aaaaagtggt taagatgggc 960
      38 cgggcatggg ggatcacgct tgcaatccca cacctttggg aggctgaggt gggtgattac 1020
      39 gaggtcagga gttcgagacc agcctgacca ccatggtgaa accccgtctc tactaaaagt 1080
      40 acaaaattag ccgggtgtcg tggcacacgt ctgtaatccc agctactggg gaggctgagt 1140
```



```
237 tgctttaagt tgaatcttta aacttatctt tatttttgag acacagtctc actctgtcgc 12960
238 ccaggctgga gtgcagtggt acaaccacag ctcagtgcag cgttgacctc ctgggctcaa 13020
239 gccatcctcc cgcctcagcc tcccgagtag ctgggactac aggcgcacac aaccatgtcc 13080
240 agcttatttt tgtatttttt gtagagacag ggtcccactg tgttgccctg gcttgttctg 13140
241 aactcctagg ctcaagtgat cccccccgcct caccctccca aagtgctggg attacaggca 13200
242 tgagccacca catccagact tcactttttt gtttaatgtc gcaaatggca taaggaatgg 13260
243 gattcaatgg ggacacattt ataaacgttg cagcagctcc tagaacttgc ctatccttgt 13320
244 aaacttctct aggtgattgc taattacttc tttttttttt ttttttttttg agacggagtc 13380
245 tcactctgtc gcccaggctg gagtacagtg gcgcaatctc gtctcactgc aaactccacc 13440
246 tcccgggttc acgccattct cctgcctcag cctcccgagt agctgggact acaggcaccc 13500
247 gccaccacgc ccggctaatt ttttgtattt tttttttagta gaggtggggt ttcactgtgt 13560
248 tatccaggat ggtcttgatc tcctgacctc gtgatccacc tgcctcagcc tcccaaagtg 13620
249 ctgggattac aggcgtgagc caccatgccc agcccgctaa ttatttcaat ttgaccttga 13680
250 cactgagcct gccaagtagg ttcaagcatt ttgatggccc ctttacaggt tgggaaagct 13740
251 aatttatctg tccaaggccg aattctgaaa ctgagtctta actgccaaaa attcttatca 13800
252 tcaatttctt cttctgggtt gggcacagtg gctcatgcct gtaaagccag caatttgaga 13860
253 ggcatcatga tgcaagagga agaggattga gtgaagctag gagtttggga ccagcctggg 13920
254 caacatagtg agaccccatc tataaaaaaa aattaaaaat tagttgggca tggtggtgca 13980
255 ctcctgtggt cctagctatt caggaggctg aggtgggagg attccttgag cccaggggttg 14040
256 acgctgcaga gagctgtgat cacgccactg cagtccagcc tgagtgacag ctggaaataa 14100
257 tgataaataa ataataaata attatttaaa aaattataat aaaaataatt aaaaaattat 14160
258 tttccctgat taatctttttt ttttgtcctt ctgagagttc aatttgtccc ttttctgcct 14220
259 ggtctcctag gtttccctaa aatcctgctg agaggttagc actgcctgcc aaagtcagtt 14280
260 tgcaaaatcc cagagaaatc cagcttattc ctgggggaac cgccaagact gcccagccct 14340
261 gtgtggggtt caggcaagtt tctcacatgt gccttttttgg caagaggcct ctggcaaccc 14400
262 catgagtccc caaagagact caattctaaa agttggtctc caccagctct ctgtggctta 14460
263 ggggttcaag ttcaactgtg aaagccctgt tttgttttga ttttgctttg agggagagga 14520
264 aaccgcccttt ctgtttgttc aactccttct cctaagggga gaaatcaata tttacgtcca 14580
265 gactccaggt atccgtacaa ttgattttttc agatgtttat actcagccaa aggcgggatc 14640
266 ccacaaaaca aaaaatattt ttttggctgt acttttgtga agattttatt taaattcctg 14700
267 attgatcagt gtctattagg tgatttggaa taacaatgta aaaacaatat acaacgaaag 14760
268 gaagctaaaa atctatacac aattcctaga aaggaaaagg caaatataga aagtggcgga 14820
269 agttcccaac atttttagtg ttttccttttt gaggcagaga ggacaatggc attaggctat 14880
270 tggaggatct tgaaaggctg ttgttatcct tctgtggaca acaacagcaa aatgttaaca 14940
271 gttaaacatc gagaaatttc aggaggatct ttcagaagat gcgtttccaa tttttgagggg 15000
272 gcgtcagctc ttcaccggag acccaaatac aacaaatcaa gtcgcctgcc ctggcgacac 15060
273 tttcgaagga ctggagtggg aatcagagct tcacgggtta aaaagccgat gtcacatcgg 15120
274 ccgttcgaaa ctcctcctct tgcagtgagg tgaagacatt tgaaaatcac cccactgcaa 15180
275 actcctcccc ctgctagaaa cctcacattg aaatgctgta aatgacgtgg gccccgagtg 15240
276 caatcgcggg aagccaggt ttccagctag dacacagcag gtcgtgatcc gggtcgggac 15300
277 actgcctggc agaggctgcg agc atg ggg ccc tgg ggc tgg aaa ttg cgc  15350
```

Met   (met)(gly)(pro)(trp) gly (trp)(lys)(leu)(arg)   ← *these are misaligned. They*

279   -21 -20   -15   *need to*

280 tgg acc gtc gcc ttg ctc ctc gcc gcg gcg ggg act gca g gtaaggcttg 15400   *be directly*

281 (trp thr val ala leu leu leu ala ala ala gly thr ala v)   *under,*

282   -10   -5   -1 1   *Codon*

```
283 ctccaggcgc cagaataggt tgagagggag cccccggggg gcccttggga atttattttt 15460
284 ttgggtacaa ataatcactc catccctggg agacttgtgg ggtaatggca cggggtcctt 15520
285 cccaaacggc tggagggggc gctggagggg ggcgctgagg ggagcgcgag ggtcgggagg 15580
```

) use upper-case for initial letter of amino acid

Met Gly Pro

atg Met

do not use TAB Codes between amino acids   7/29/05

```
     1176 agtagctggg gccacaggcg cctgccacca cgcccggcta attttttttt gtacttcttt 59327
     1177 tagtacagac ggggtttcac catgttagcc aggatggtct cgatctcctg accttgtgat 59387
     1178 ccacctgctt cggcctccca aagtgctgag attacaggcg tgagccaccg cgggtggcca 59447
     1179 acgctaattt ttttgttttt ttagatggag tcttgctctg tcgcccaggc tggagtgcag 59507
     1180 tggcgtgatc tctgcctact gcaagctccg cctcccgggt tcatgccatt ctcctgcctc 59567
     1181 agcctcctga gtaactggga ctacaggcac ccgccaccac gcccggctaa ttttttgtat 59627
     1182 ttttagtaga gacagggttt caccgtgtta gccaggatgg tcttgatctc ctgaccttgt 59687
     1183 gatccacccg tctcggcctc ccaaagtgct gggattagag gtgtgagcca ccacacctgg 59747
     1184 cctagcctgg ctaatttttg tatttttggt agagacgggg tttcaccatg ttggtcaggc 59807
     1185 tggtcttgaa cttctgacct caggtaatct gcctgcctca gtctcccaaa gtgctgggat 59867
     1186 tacaggtgtg agccaccgcg cctggcctca cttccttctg tcatctgttt gtggattgga 59927
     1187 ctccccagga gaaggaccca gaaggggaag actcccagaa ctccgggcaa gatgcaatct 59987
     1188 ccgtgggctg cca        60000
E--> 1190 <210>       SEQ ID NO: 2          ) delete
     1191 <211> LENGTH: 24
E--> 1192 <212> TYPE: polynucleotide  invalid
     1193 <213> ORGANISM: artificial sequence
W--> 1194 <220> FEATURE:
W--> 1195 <221> NAME/KEY: oligonucleotide      give source of genetic material
     1196 <223> OTHER INFORMATION: Ex1F       (see item 11 on
W--> 1197 <400> SEQUENCE: 24←insert           Error summary
     1198 cacattgaaa tgctgtaaat gacg   24←insert   sheet)
E--> 1200 <210> SEQ ID NO: SEQ ID NO: 3    cumulative
     1201 <211> LENGTH: 24                  base total
E--> 1202 <212> TYPE: polynucleotide       at right
     1203 <213> ORGANISM: artificial sequence   margin of
W--> 1204 <220> FEATURE:                   each line
W--> 1205 <221> NAME/KEY: oligonucleotide
     1206 <223> OTHER INFORMATION: Ex1R
E--> 1209 <400> SEQUENCE:
     1210 ctattctggc gcctggagca agcc
E--> 1212 <210> SEQ ID NO: SEQ ID NO: 4
     1213 <211> LENGTH: 24
E--> 1214 <212> TYPE: polynucleotide
     1215 <213> ORGANISM: artificial sequence
W--> 1216 <220> FEATURE:
W--> 1217 <221> NAME/KEY: oligonucleotide
     1218 <223> OTHER INFORMATION: Ex2F
W--> 1219 <400> SEQUENCE:
     1220 ttgagagacc ctttctcctt ttcc
E--> 1222 <210> SEQ ID NO: SEQ ID NO: 5
     1223 <211> LENGTH: 20
E--> 1224 <212> TYPE: polynucleotide
     1225 <213> ORGANISM: artificial sequence
W--> 1226 <220> FEATURE:
W--> 1227 <221> NAME/KEY: oligonucleotide
     1228 <223> OTHER INFORMATION: Ex2R
W--> 1229 <400> SEQUENCE:
     1230 gcatatcatg cccaaagggg
```

fix these errors

```
E--> 1506 <212> TYPE: polynucleotide
     1507 <213> ORGANISM: artificial sequence
W--> 1508 <220> FEATURE:
W--> 1509 <221> NAME/KEY: oligonucleotide
     1510 <223> OTHER INFORMATION: Ex15R
W--> 1511 <400> SEQUENCE:
     1512 tagggagggc ccagtcttt
E--> 1514 <210> SEQ ID NO: SEQ ID NO: 34
     1515 <211> LENGTH: 20
E--> 1516 <212> TYPE: polynucleotide
     1517 <213> ORGANISM: artificial sequence
W--> 1518 <220> FEATURE:
W--> 1519 <221> NAME/KEY: oligonucleotide
     1520 <223> OTHER INFORMATION: Ex17F
W--> 1521 <400> SEQUENCE:
     1522 gggtctctgg tctcgggggc
E--> 1524 <210> SEQ ID NO: SEQ ID NO: 35
     1525 <211> LENGTH: 22
E--> 1526 <212> TYPE: polynucleotide
     1527 <213> ORGANISM: artificial sequence
W--> 1528 <220> FEATURE:
W--> 1529 <221> NAME/KEY: oligonucleotide
     1530 <223> OTHER INFORMATION: Ex17R
W--> 1531 <400> SEQUENCE:
     1532 ggctctggct ttctagagag gg
E--> 1534 <210> SEQ ID NO: SEQ ID NO: 36
     1535 <211> LENGTH: 23
E--> 1536 <212> TYPE: polynucleotide
     1537 <213> ORGANISM: artificial sequence
W--> 1538 <220> FEATURE:
W--> 1539 <221> NAME/KEY: oligonucleotide
W--> 1540 <223> OTHER INFORMATION:
W--> 1540 <400> SEQUENCE:
     1541 cgggtcggga cactgcctgg cag
E--> 1544 <210> SEQ ID NO: SEQ ID NO: 37
     1545 <211> LENGTH: 23
E--> 1546 <212> TYPE: polynucleotide
     1547 <213> ORGANISM: artificial sequence
W--> 1548 <220> FEATURE:
W--> 1549 <221> NAME/KEY: oligonucleotide
W--> 1550 <223> OTHER INFORMATION:
W--> 1550 <400> SEQUENCE:
     1551 cgggtcggga ccctgcctgg cag
E--> 1553 <210> SEQ ID NO: SEQ ID NO: 38
     1554 <211> LENGTH: 23
E--> 1555 <212> TYPE: polynucleotide
     1556 <213> ORGANISM: artificial sequence
W--> 1557 <220> FEATURE:
W--> 1558 <221> NAME/KEY: oligonucleotide
```

[handwritten annotations:]

← mandatory response needed on <223> line

Artificial sequence MUST be explained on <223> line

These pages are shown as samples of global error. Please consult sequence Rules and attached sample sequence listing for valid format.

<110>   Smith, John; Smithgene Inc.

<120>   Example of a Sequence Listing

<130>   01-00001

<140>   PCT/EP98/00001
<141>   1998-12-31

<150>   US 08/999,999
<151>   1997-10-15

<160>   4

<170>   PatentIn version 2.0

<210>   1
<211>   389
<212>   DNA
<213>   Paramecium sp.

<220>
<221>   CDS
<222>   (279)...(389)

<300>
<301>   Doe, Richard
<302>   Isolation and Characterization of a Gene Encoding a
         Protease from Paramecium sp.
<303>   Journal of Genes
<304>   1
<305>   4
<306>   1-7
<307>   1988-06-31
<308>   123456
<309>   1988-06-31

<400>   1
agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc   60

agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc   120

tgatgtggca attgctggca gtgccacagg cttttcagcc aggcttaggg tgggttccgc   180

cgcggcgcgg cggcccctct cgcgctcctc tcgcgcctct ctctcgctct cctctcgctc   240

	ggacctgatt	aggtgagcag	gaggagggg	cagttagc	atg	gtt	tca	atg	ttc	agc	296
					Met	Val	Ser	Met	Phe	Ser	
					1				5		

ttg	tct	ttc	aaa	tgg	cct	gga	ttt	tgt	ctg	ttt	gtt	tgt	ttg	ttc	caa	344
Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	Phe	Val	Cys	Leu	Phe	Gln	
			10					15					20			

tgt	ccc	aaa	gtc	ctc	ccc	tgt	cac	tca	tca	ctg	cag	ccg	aat	ctt		389
Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	Leu	Gln	Pro	Asn	Leu		
		25					30					35				

<210>   2
<211>   37
<212>   PRT
<213>   Paramecium sp.

<400>   2
Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu
1				5					10					15	

Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser
			20					25					30		

Leu	Gln	Pro	Asn	Leu
		35		

<210>   3
<211>   11
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Designed peptide based on size and polarity to act as a
         linker between the alpha and beta chains of Protein XYZ.

<400>   3
Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile
1				5					10	

<210>   4
<400>   4
000

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

		Whether presented sequence mole-cule is DNA, RNA, or PRT (protein). If a nucleotide sequence con-tains both DNA and RNA frag-ments, the type shall be "DNA." In ad-dition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<212>	Type		
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artifi-cial Sequence. In addition, the "Unknown" or "Artificial Se-quence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of bio-logical signi-ficance in the sequence.	M, under the following condi-tions: if "n," "Xaa," or a mod-ified or unusual L-amino acid or modified base was used in a se-quence; if ORGAN-ISM is "Artifi-cial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, pre-ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the fol-lowing conditions: if "n," "Xaa," or a modified or un-usual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the fol-lowing conditions: if "n," "Xaa," or a modified or un-usual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other information	Other relevant information; four lines maximum	M under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line pre-ceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;